Serial Number: _09/155,514A_

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:

_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

_____

☑ Inserted or corrected a nucleic number at the end of a nucleic line.   SEQ ID NO's edited: _1_

_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:

_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:

_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:

_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:

_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:

_____

_____

_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING   DATE: 07/21/2000
PATENT APPLICATION: US/09/155,514A   TIME: 13:05:13

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07212000\I155514A.raw

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      3 <110> APPLICANT: Kainoh, Mie
      4        Tanaka, Toshiaki
W--> 5 <120> TITLE OF INVENTION: Chimeric proteins, their heterodimer complexes, and platelet
W--> 6       substitutes
W--> 7 <130> FILE REFERENCE: 1102-98
W--> 8 <140> CURRENT APPLICATION NUMBER: US/09/155,514A
C--> 8 <141> CURRENT FILING DATE: 1998-11-17
      9 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00370
     10 <151> PRIOR FILING DATE: 1997-01-29
     11 <150> PRIOR APPLICATION NUMBER: JP 9-15118
     12 <151> PRIOR FILING DATE: 1997-01-29
     13 <150> PRIOR APPLICATION NUMBER: JP 9-234544
     14 <151> PRIOR FILING DATE: 1997-08-29
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     16 <170> SOFTWARE: Microsoft Word 2000
     18 <210> SEQ ID NO: 1
     19 <211> LENGTH: 4228
     20 <212> TYPE: DNA
     21 <213> ORGANISM: Homo sapien
     23 <220> FEATURE:
     24 <221> NAME/KEY: CDS
     25 <222> LOCATION: 1...2958, 3316...3360, 3480...3808, 3905...4228
     27 <400> SEQUENCE: 1
     28 atg ttc ccc acc gag agc gca tgg ctt ggg aag cga ggc gcg aac ccg      48
     29 Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro
     30                 -35                 -30                 -25
     31 ggc ccc gaa gct gca ctc cgg gag acg gtg atg ctg ttg ctg tgc ctg      96
     32 Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Leu Cys Leu
     33                 -20                 -15                 -10
     34 ggg gtc ccg acc ggc agg cct tac aac gtg gac act gag agc gcg ctg     144
     35 Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
     36                 -5                   1                   5
     37 ctt tac cag ggc ccc cac aac acg ctg ttc ggc tac tcg gtc gtg ctg     192
     38 Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
     39 10                  15                  20                  25
     40 cac agc cac ggg gcg aac cga tgg ctc cta gtg ggt gcg ccc act gcc     240
     41 His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala
     42                 30                  35                  40
     43 aac tgg ctc gcc aac gct tca gtg atc aat ccc ggg gcg att tac aga     288
     44 Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg
     45                 45                  50                  55
     46 tgc acg atc gga aag aat ccc ggc cag acg tgc gaa cag ctc cag ctg     336
     47 Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu
     48         60                  65                  70
     49 ggt agc cct aat gga gaa cct tgt gga aag act tgt ttg gaa gag aga     384
     50 Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg
     51      75                  80                  85
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RAW SEQUENCE LISTING   DATE: 07/21/2000
PATENT APPLICATION: US/09/155,514A   TIME: 13:05:13

Input Set : A:\Pto.amc
Output Set: N:\CRF3\07212000\I155514A.raw

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52 gac aat cag tgg ttg ggg gtc aca ctt tcc aga cag cca gga gaa aat    432
53 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn
54  90                   95                  100                 105
55 gga tcc atc gtg act tgt ggg cat aga tgg aaa aat ata ttt tac ata    480
56 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile
57              110                 115                 120
58 aag aat gaa aat aag ctc ccc act ggt ggt tgc tat gga gtg ccc cct    528
59 Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro
60              125                 130                 135
61 gat tta cga aca gaa ctg agt aaa aga ata gct ccg tgt tat caa gat    576
62 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp
63          140                 145                 150
64 tat gtg aaa aaa ttt gga gaa aat ttt gca tca tgt caa gct gga ata    624
65 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile
66      155                 160                 165
67 tcc agt ttt tac aca aag gat tta att gtg atg ggg gcc cca gga tca    672
68 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser
69 170                 175                 180                 185
70 tct tac tgg act ggc tct ctt ttt gtc tac aat ata act aca aat aaa    720
71 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys
72      .           190                 195                 200
73 tac aag gct ttt tta gac aaa caa aat caa gta aaa ttt gga agt tat    768
74 Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr
75              205                 210                 215
76 tta gga tat tca gtc gga gct ggt cat ttt cgg agc cag cat act acc    816
77 Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr
78      220                 225                 230
79 gaa gta gtc gga gga gct cct caa cat gag cag att ggt aag gca tat    864
80 Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr
81      235                 240                 245
82 ata ttc agc att gat gaa aaa gaa cta aat atc tta cat gaa atg aaa    912
83 Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys
84 250                 255                 260                 265
85 ggt aaa aag ctt gga tcg tac ttt gga gct tct gtc tgt gct gtg gac    960
86 Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp
87              270                 275                 280
88 ctc aat gca gat ggc ttc tca gat ctg ctc gtg gga gca ccc atg cag   1008
89 Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln
90              285                 290                 295
91 agc acc atc aga gag gaa gga aga gtg ttt gtg tac atc aac tct ggc   1056
92 Ser Thr Ile Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly
93      300                 305                 310
94 tcg gga gca gta atg aat gca atg gaa aca aac ctc gtt gga agt gac   1104
95 Ser Gly Ala Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp
96      315                 320                 325
97 aaa tat gct gca aga ttt ggg gaa tct ata gtt aat ctt ggc gac att   1152
98 Lys Tyr Ala Ala Arg Phe Gly Glu Ser Ile Val Asn Leu Gly Asp Ile
99 330                 335                 340                 345
100 gac aat gat ggc ttt gaa gat gtt gct atc gga gct cca caa gaa gat   1200
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101 Asp Asn Asp Gly Phe Glu Asp Val Ala Ile Gly Ala Pro Gln Glu Asp
102                 350             355             360
103 gac ttg caa ggt gct att tat att tac aat ggc cgt gca gat ggg atc   1248
104 Asp Leu Gln Gly Ala Ile Tyr Ile Tyr Asn Gly Arg Ala Asp Gly Ile
105             365             370             375
106 tcg tca acc ttc tca cag aga att gaa gga ctt cag atc agc aaa tcg   1296
107 Ser Ser Thr Phe Ser Gln Arg Ile Glu Gly Leu Gln Ile Ser Lys Ser
108             380             385             390
109 tta agt atg ttt gga cag tct ata tca gga caa att gat gca gat att   1344
110 Leu Ser Met Phe Gly Gln Ser Ile Ser Gly Gln Ile Asp Ala Asp Asn
111     395             400             405
112 aat ggc tat gta gat gta gca ggt cgt gct ttt cgg tct gat tct gct   1392
113 Asn Gly Tyr Val Asp Val Ala Val Gly Ala Phe Arg Ser Asp Ser Ala
114 410             415             420             425
115 gtc ttg cta agg aca aga cct gta gta att gtt gac gct tct tta agc   1440
116 Val Leu Leu Arg Thr Arg Pro Val Val Ile Val Asp Ala Ser Leu Ser
117             430             435             440
118 cac cct gag tca gta aat aga acg aaa ttt gac tgt gtt gaa aat gga   1488
119 His Pro Glu Ser Val Asn Arg Thr Lys Phe Asp Cys Val Glu Asn Gly
120         445             450             455
121 tgg cct tct gtg tgc ata gat cta aca ctt tgt ttc tca tat aag ggc   1536
122 Trp Pro Ser Val Cys Ile Asp Leu Thr Leu Cys Phe Ser Tyr Lys Gly
123         460             465             470
124 aag gaa gtt cca ggt tac att gtt ttg ttt tat aac atg agt ttg gat   1584
125 Lys Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp
126     475             480             485
127 gtg aac aga aag gca gag tct cca cca aga ttc tat ttc tct tct aat   1632
128 Val Asn Arg Lys Ala Glu Ser Pro Pro Arg Phe Tyr Phe Ser Ser Asn
129 490             495             500             505
130 gga act tct gac gtg att aca gga agc ata cag gtg tcc agc aga gaa   1680
131 Gly Thr Ser Asp Val Ile Thr Gly Ser Ile Gln Val Ser Ser Arg Glu
132             510             515             520
133 gct aac tgt aga aca cat caa gca ttt atg cgg aaa gat gtg cgg gac   1728
134 Ala Asn Cys Arg Thr His Gln Ala Phe Met Arg Lys Asp Val Arg Asp
135         525             530             535
136 atc ctc acc cca att cag att gaa gct gct tac cac ctt ggt cct cat   1776
137 Ile Leu Thr Pro Ile Gln Ile Glu Ala Ala Tyr His Leu Gly Pro His
138         540             545             550
139 gtc atc agt aaa cga agt aca gag gaa ttc cca cca ctt cag cca att   1824
140 Val Ile Ser Lys Arg Ser Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile
141 555             560             565
142 ctt cag cag aag aaa gaa aaa gac ata atg aaa aaa aca ata aac ttt   1872
143 Leu Gln Gln Lys Lys Glu Lys Asp Ile Met Lys Lys Thr Ile Asn Phe
144 570             575             580             585
145 gca agg ttt tgt gcc cat gaa aat tgt tct gct gat tta cag gtt tct   1920
146 Ala Arg Phe Cys Ala His Glu Asn Cys Ser Ala Asp Leu Gln Val Ser
147         590             595             600
148 gca aag att ggg ttt ttg aag ccc cat gaa aat aaa aca tat ctt gct   1968
149 Ala Lys Ile Gly Phe Leu Lys Pro His Glu Asn Lys Thr Tyr Leu Ala
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150             605             610             615
151 gtt ggg agt atg aag aca ttg atg ttg aat gtg tcc ttg ttt aat gct    2016
152 Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu Phe Asn Ala
153             620             625             630
154 gga gat gat gca tat gaa acg act cta cat gtc aaa cta ccc gtg ggt    2064
155 Gly Asp Asp Ala Tyr Glu Thr Thr Leu His Val Lys Leu Pro Val Gly
156     635             640             645
157 ctt tat ttc att aag att tta gag ctg gaa gag aag caa ata aac tgt    2112
158 Leu Tyr Phe Ile Lys Ile Leu Glu Leu Glu Glu Lys Gln Ile Asn Cys
159 650             655             660             665
160 gaa gtc aca gat aac tct ggc gtg gta caa ctt gac tgc agt att ggc    2160
161 Glu Val Thr Asp Asn Ser Gly Val Val Gln Leu Asp Cys Ser Ile Gly
162             670             675             680
163 tat ata tat gta gat cat ctc tca agg ata gat att agc ttt ctc ctg    2208
164 Tyr Ile Tyr Val Asp His Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu
165             685             690             695
166 gat gtg agc tca ctc agc aga gcg gaa gag gac ctc agt atc aca gtg    2256
167 Asp Val Ser Ser Leu Ser Arg Ala Glu Glu Asp Leu Ser Ile Thr Val
168             700             705             710
169 cat gct acc tgt gaa aat gaa gag gaa atg gac aat cta aag cac agc    2304
170 His Ala Thr Cys Glu Asn Glu Glu Glu Met Asp Asn Leu Lys His Ser
171     715             720             725
172 aga gtg act gta gca ata cct tta aaa tat gag gtt aag ctg act gtt    2352
173 Arg Val Thr Val Ala Ile Pro Leu Lys Tyr Glu Val Lys Leu Thr Val
174 730             735             740             745
175 cat ggg ttt gta aac cca act tca ttt gtg tat gga tca aat gat gaa    2400
176 His Gly Phe Val Asn Pro Thr Ser Phe Val Tyr Gly Ser Asn Asp Glu
177             750             755             760
178 aat gag cct gaa acg tgc atg gtg gag aaa atg aac tta act ttc cat    2448
179 Asn Glu Pro Glu Thr Cys Met Val Glu Lys Met Asn Leu Thr Phe His
180             765             770             775
181 gtt atc aac act ggc aat agt atg gct ccc aat gtt agt gtg gaa ata    2496
182 Val Ile Asn Thr Gly Asn Ser Met Ala Pro Asn Val Ser Val Glu Ile
183             780             785             790
184 atg gta cca aat tct ttt agc ccc caa act gat aag ctg ttc aac att    2544
185 Met Val Pro Asn Ser Phe Ser Pro Gln Thr Asp Lys Leu Phe Asn Ile
186     795             800             805
187 ttg gat gtc cag act act act gga gaa tgc cac ttt gaa aat tat caa    2592
188 Leu Asp Val Gln Thr Thr Thr Gly Glu Cys His Phe Glu Asn Tyr Gln
189 810             815             820             825
190 aga gtg tgt gca tta gag cag caa aag agt gca atg cag acc ttg aaa    2640
191 Arg Val Cys Ala Leu Glu Gln Gln Lys Ser Ala Met Gln Thr Leu Lys
192             830             835             840
193 ggc ata gtc cgg ttc ttg tcc aag act gat aag agg cta ttg tac tgc    2688
194 Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys
195             845             850             855
196 ata aaa gct gat cca cat tgt tta aat ttc ttg tgt aat ttt ggg aaa    2736
197 Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys
198     860             865             870
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              RAW SEQUENCE LISTING                    DATE: 07/21/2000
              PATENT APPLICATION:  US/09/155,514A     TIME: 13:05:13

              Input Set : A:\Pto.amc
              Output Set: N:\CRF3\07212000\I155514A.raw


199 atg gaa agt gga aaa gaa gcc agt gtt cat atc caa ctg gaa ggc cgg    2784
200 Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg
201     875                 880                 885
202 cca tcc att tta gaa atg gat gag act tca gca ctc aag ttt gaa ata    2832
203 Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile
204 890                 895                 900                 905
205 aga gca aca ggt ttt cca gag cca aat cca aga gta att gaa cta aac    2880
206 Arg Ala Thr Gly Phe Pro Glu Pro Asn Pro Arg Val Ile Glu Leu Asn
207                 910                 915                 920
208 aag gat gag aat gtt gcg cat gtt cta ctg gaa gga cta cat cat caa    2928
209 Lys Asp Glu Asn Val Ala His Val Leu Leu Glu Gly Leu His His Gln
210                 925                 930                 935
211 aga ccc aaa cgt tat ttc acg gat ccc gag ctgctggaag caggctcagc      2978
212 Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu
213       940                 945
214 gctcctgcct ggacgcatcc cggctatgca gccccagtcc agggcagcaa ggcaggcccc  3038
215 gtctgcctct tcacccggag cctctgcccg ccccactcat gctcagggag agggtcttct  3098
216 ggctttttcc caggctctgg gcaggcacag gctaggtgcc cctaacccag gccctgcaca  3158
217 caaaggggca ggtgctgggc tcagacctgc aagagccat atccgggagg accctgcccc   3218
218 tgacctaagc ccaccccaaa ggccaaactc tccactccct cagctcggac accttctctc  3278
219 ctcccagatt ccagtaactc ccaatcttct ctctgca gag ccc aaa tct tgt gac   3333
220                                              Glu Pro Lys Ser Cys Asp
221                                                          950
222 aaa act cac aca tgc cca ccg tgc cca ggtaagccag cccaggcctc          3380
223 Lys Thr His Thr Cys Pro Pro Cys Pro
224     955                 960
225 gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcatccagg gacaggcccc  3440
226 agccgggtgc tgacacgtcc acctccatct cttcctca gca cct gaa ctc ctg      3493
227                                              Ala Pro Glu Leu Leu
228                                                          965
229 ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc    3541
230 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
231             970                 975                 980
232 atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc    3589
233 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
234     985                 990                 995
235 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag    3637
236 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
237 1000                1005                1010                1015
238 gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg    3685
239 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
240                 1020                1025                1030
241 tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat    3733
242 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
243             1035                1040                1045
244 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc    3781
245 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
246     1050                1055                1060
247 atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtggggtgcg          3828
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                      VERIFICATION SUMMARY              DATE: 07/21/2000
                      PATENT APPLICATION:  US/09/155,514A    TIME: 13:05:14

                      Input Set  : A:\Pto.amc
                      Output Set: N:\CRF3\07212000\I155514A.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:282 W: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:283 W: Missing Blank Line separator, <160> field identifier
L:505 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:507 M:283 W: Missing Blank Line separator, <400> field identifier
L:516 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:528 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:541 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:554 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:566 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:578 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:590 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:602 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:612 M:283 W: Missing Blank Line separator, <220> field identifier
L:613 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:615 M:283 W: Missing Blank Line separator, <400> field identifier
L:625 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:637 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:651 M:283 W: Missing Blank Line separator, <400> field identifier
L:660 M:283 W: Missing Blank Line separator, <220> field identifier
L:660 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:663 M:283 W: Missing Blank Line separator, <400> field identifier
L:672 M:283 W: Missing Blank Line separator, <220> field identifier
L:672 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:968 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:980 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:992 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:1004 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:1041 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
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1644

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RAW SEQUENCE LISTING                    DATE: 07/18/2000
PATENT APPLICATION:  US/09/155,514A     TIME: 13:51:00

Input Set : A:\09155514.app
Output Set: N:\CRF3\07182000\I155514A.raw
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       3 <110> APPLICANT: Kainoh, Mie
       4        Tanaka, Toshiaki
W-->   5 <120> TITLE OF INVENTION: Chimeric proteins, their heterodimer complexes, and platelet
W-->   6        substitutes
W-->   7 <130> FILE REFERENCE: 1102-98
W-->   8 <140> CURRENT APPLICATION NUMBER: US/09/155,514A
C-->   8 <141> CURRENT FILING DATE: 1998-11-17
       9 <150> PRIOR APPLICATION NUMBER: PCT/JP98/00370
      10 <151> PRIOR FILING DATE: 1997-01-29
      11 <150> PRIOR APPLICATION NUMBER: JP 9-15118
      12 <151> PRIOR FILING DATE: 1997-01-29
      13 <150> PRIOR APPLICATION NUMBER: JP 9-234544
      14 <151> PRIOR FILING DATE: 1997-08-29
W-->  15 <160> NUMBER OF SEQ ID: 34
      16 <170> SOFTWARE: Microsoft Word 2000


ERRORED SEQUENCES

      18 <210> SEQ ID NO: 1
      19 <211> LENGTH: 4228
      20 <212> TYPE: DNA
      21 <213> ORGANISM: Homo sapien
      23 <220> FEATURE:
      24 <221> NAME/KEY: CDS
      25 <222> LOCATION: 1...2958, 3316...3360, 3480...3808, 3905...4228
      27 <400> SEQUENCE: 1
      28 atg ttc ccc acc gag agc gca tgg ctt ggg aag cga ggc gcg aac ccg      48
      29 Met Phe Pro Thr Glu Ser Ala Trp Leu Gly Lys Arg Gly Ala Asn Pro
      30               -35               -30                  -25
      31 ggc ccc gaa gct gca ctc cgg gag acg gtg atg ctg ttg ctg tgc ctg      96
      32 Gly Pro Glu Ala Ala Leu Arg Glu Thr Val Met Leu Leu Leu Cys Leu
      33              -20               -15                  -10
      34 ggg gtc ccg acc ggc agg cct tac aac gtg gac act gag agc gcg ctg     144
      35 Gly Val Pro Thr Gly Arg Pro Tyr Asn Val Asp Thr Glu Ser Ala Leu
      36             -5                 1                 5
      37 ctt tac cag ggc ccc cac aac acg ctg ttc ggc tac tcg gtc gtg ctg     192
      38 Leu Tyr Gln Gly Pro His Asn Thr Leu Phe Gly Tyr Ser Val Val Leu
      39 10                  15                  20                  25
      40 cac agc cac ggg gcg aac cga tgg ctc cta gtg ggt gcg ccc act gcc     240
      41 His Ser His Gly Ala Asn Arg Trp Leu Leu Val Gly Ala Pro Thr Ala
      42                  30                  35                  40
      43 aac tgg ctc gcc aac gct tca gtg atc aat ccc ggg gcg att tac aga     288
      44 Asn Trp Leu Ala Asn Ala Ser Val Ile Asn Pro Gly Ala Ile Tyr Arg
      45                  45                  50                  55
      46 tgc acg atc gga aag aat ccc ggc cag acg tgc gaa cag ctc cag ctg     336
      47 Cys Arg Ile Gly Lys Asn Pro Gly Gln Thr Cys Glu Gln Leu Gln Leu
```

```
48          60                   65                 70
49 ggt agc cct aat gga gaa cct tgt gga aag act tgt ttg gaa gag aga        384
50 Gly Ser Pro Asn Gly Glu Pro Cys Gly Lys Thr Cys Leu Glu Glu Arg
51       75                   80                 85
52 gac aat cag tgg ttg ggg gtc aca ctt tcc aga cag cca gga gaa aat        432
53 Asp Asn Gln Trp Leu Gly Val Thr Leu Ser Arg Gln Pro Gly Glu Asn
54  90                   95                  100                105
55 gga tcc atc gtg act tgt ggg cat aga tgg aaa aat ata ttt tac ata        480
56 Gly Ser Ile Val Thr Cys Gly His Arg Trp Lys Asn Ile Phe Tyr Ile
57               110                  115                120
58 aag aat gaa aat aag ctc ccc act ggt ggt tgc tat gga gtg ccc cct        528
59 Lys Asn Glu Asn Lys Leu Pro Thr Gly Gly Cys Tyr Gly Val Pro Pro
60               125                  130                135
61 gat tta cga aca gaa ctg agt aaa aga ata gct ccg tgt tat caa gat        576
62 Asp Leu Arg Thr Glu Leu Ser Lys Arg Ile Ala Pro Cys Tyr Gln Asp
63          140                  145                150
64 tat gtg aaa aaa ttt gga gaa aat ttt gca tca tgt caa gct gga ata        624
65 Tyr Val Lys Lys Phe Gly Glu Asn Phe Ala Ser Cys Gln Ala Gly Ile
66       155                  160                  165
67 tcc agt ttt tac aca aag gat tta att gtg atg ggg gcc cca gga tca        672
68 Ser Ser Phe Tyr Thr Lys Asp Leu Ile Val Met Gly Ala Pro Gly Ser
69 170                  175                  180                185
70 tct tac tgg act ggc tct ctt ttt gtc tac aat ata act aca aat aaa        720
71 Ser Tyr Trp Thr Gly Ser Leu Phe Val Tyr Asn Ile Thr Thr Asn Lys
72               190                  195                200
73 tac aag gct ttt tta gac aaa caa aat caa gta aaa ttt gga agt tat        768
74 Tyr Lys Ala Phe Leu Asp Lys Gln Asn Gln Val Lys Phe Gly Ser Tyr
75          205                  210                  215
76 tta gga tat tca gtc gga gct ggt cat ttt cgg agc cag cat act acc        816
77 Leu Gly Tyr Ser Val Gly Ala Gly His Phe Arg Ser Gln His Thr Thr
78          220                  225                  230
79 gaa gta gtc gga gga gct cct caa cat gag cag att ggt aag gca tat        864
80 Glu Val Val Gly Gly Ala Pro Gln His Glu Gln Ile Gly Lys Ala Tyr
81       235                  240                  245
82 ata ttc agc att gat gaa aaa gaa cta aat atc tta cat gaa atg aaa        912
83 Ile Phe Ser Ile Asp Glu Lys Glu Leu Asn Ile Leu His Glu Met Lys
84 250                  255                  260                265
85 ggt aaa aag ctt gga tcg tac ttt gga gct tct gtc tgt gct gtg gac        960
86 Gly Lys Lys Leu Gly Ser Tyr Phe Gly Ala Ser Val Cys Ala Val Asp
87               270                  275                280
88 ctc aat gca gat ggc ttc tca gat ctg ctc gtg gga gca ccc atg cag       1008
89 Leu Asn Ala Asp Gly Phe Ser Asp Leu Leu Val Gly Ala Pro Met Gln
90               285                  290                295
91 agc acc atc aga gag gaa gga aga gtg ttt gtg tac atc aac tct ggc       1056
92 Ser Thr Ile Arg Glu Glu Gly Arg Val Phe Val Tyr Ile Asn Ser Gly
93          300                  305                  310
94 tcg gga gca gta atg aat gca atg gaa aca aac ctc gtt gga agt gac       1104
95 Ser Gly Ala Val Met Asn Ala Met Glu Thr Asn Leu Val Gly Ser Asp
96       315                  320                  325
```

RAW SEQUENCE LISTING   DATE: 07/18/2000
PATENT APPLICATION: US/09/155,514A   TIME: 13:51:00

Input Set : A:\09155514.app
Output Set: N:\CRF3\07182000\I155514A.raw

```
97  aaa tat gct gca aga ttt ggg gaa tct ata gtt aat ctt ggc gac att   1152
98  Lys Tyr Ala Ala Arg Phe Gly Glu Ser Ile Val Asn Leu Gly Asp Ile
99  330             335             340                 345
100 gac aat gat ggc ttt gaa gat gtt gct atc gga gct cca caa gaa gat   1200
101 Asp Asn Asp Gly Phe Glu Asp Val Ala Ile Gly Ala Pro Gln Glu Asp
102             350             355                 360
103 gac ttg caa ggt gct att tat att tac aat ggc cgt gca gat ggg atc   1248
104 Asp Leu Gln Gly Ala Ile Tyr Ile Tyr Asn Gly Arg Ala Asp Gly Ile
105             365             370             375
106 tcg tca acc ttc tca cag aga att gaa gga ctt cag atc agc aaa tcg   1296
107 Ser Ser Thr Phe Ser Gln Arg Ile Glu Gly Leu Gln Ile Ser Lys Ser
108             380             385                 390
109 tta agt atg ttt gga cag tct ata tca gga caa att gat gca gat att   1344
110 Leu Ser Met Phe Gly Gln Ser Ile Ser Gly Gln Ile Asp Ala Asp Asn
111     395             400             405
112 aat ggc tat gta gat gta gca ggt cgt gct ttt cgg tct gat tct gct   1392
113 Asn Gly Tyr Val Asp Val Ala Val Gly Ala Phe Arg Ser Asp Ser Ala
114 410                 415             420                 425
115 gtc ttg cta agg aca aga cct gta gta att gtt gac gct tct tta agc   1440
116 Val Leu Leu Arg Thr Arg Pro Val Val Ile Val Asp Ala Ser Leu Ser
117             430             435                 440
118 cac cct gag tca gta aat aga acg aaa ttt gac tgt gtt gaa aat gga   1488
119 His Pro Glu Ser Val Asn Arg Thr Lys Phe Asp Cys Val Glu Asn Gly
120             445             450                 455
121 tgg cct tct gtg tgc ata gat cta aca ctt tgt ttc tca tat aag ggc   1536
122 Trp Pro Ser Val Cys Ile Asp Leu Thr Leu Cys Phe Ser Tyr Lys Gly
123             460             465                 470
124 aag gaa gtt cca ggt tac att gtt ttg ttt tat aac atg agt ttg gat   1584
125 Lys Glu Val Pro Gly Tyr Ile Val Leu Phe Tyr Asn Met Ser Leu Asp
126     475             480             485
127 gtg aac aga aag gca gag tct cca cca aga ttc tat ttc tct tct aat   1632
128 Val Asn Arg Lys Ala Glu Ser Pro Pro Arg Phe Tyr Phe Ser Ser Asn
129 490             495             500                 505
130 gga act tct gac gtg att aca gga agc ata cag gtg tcc agc aga gaa   1680
131 Gly Thr Ser Asp Val Ile Thr Gly Ser Ile Gln Val Ser Ser Arg Glu
132             510             515                 520
133 gct aac tgt aga aca cat caa gca ttt atg cgg aaa gat gtg cgg gac   1728
134 Ala Asn Cys Arg Thr His Gln Ala Phe Met Arg Lys Asp Val Arg Asp
135             525             530                 535
136 atc ctc acc cca att cag att gaa gct gct tac cac ctt ggt cct cat   1776
137 Ile Leu Thr Pro Ile Gln Ile Glu Ala Ala Tyr His Leu Gly Pro His
138             540             545                 550
139 gtc atc agt aaa cga agt aca gag gaa ttc cca cca ctt cag cca att   1824
140 Val Ile Ser Lys Arg Ser Thr Glu Glu Phe Pro Pro Leu Gln Pro Ile
141     555             560                 565
142 ctt cag cag aag aaa gaa aaa gac ata atg aaa aaa aca ata aac ttt   1872
143 Leu Gln Gln Lys Lys Glu Lys Asp Ile Met Lys Lys Thr Ile Asn Phe
144 570             575             580                 585
145 gca agg ttt tgt gcc cat gaa aat tgt tct gct gat tta cag gtt tct   1920
```

```
146 Ala Arg Phe Cys Ala His Glu Asn Cys Ser Ala Asp Leu Gln Val Ser
147         590                 595                 600
148 gca aag att ggg ttt ttg aag ccc cat gaa aat aaa aca tat ctt gct   1968
149 Ala Lys Ile Gly Phe Leu Lys Pro His Glu Asn Lys Thr Tyr Leu Ala
150         605                 610                 615
151 gtt ggg agt atg aag aca ttg atg ttg aat gtg tcc ttg ttt aat gct   2016
152 Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu Phe Asn Ala
153         620                 625                 630
154 gga gat gat gca tat gaa acg act cta cat gtc aaa cta ccc gtg ggt   2064
155 Gly Asp Asp Ala Tyr Glu Thr Thr Leu His Val Lys Leu Pro Val Gly
156         635                 640                 645
157 ctt tat ttc att aag att tta gag ctg gaa gag aag caa ata aac tgt   2112
158 Leu Tyr Phe Ile Lys Ile Leu Glu Leu Glu Glu Lys Gln Ile Asn Cys
159 650                 655                 660                 665
160 gaa gtc aca gat aac tct ggc gtg gta caa ctt gac tgc agt att ggc   2160
161 Glu Val Thr Asp Asn Ser Gly Val Val Gln Leu Asp Cys Ser Ile Gly
162                 670                 675                 680
163 tat ata tat gta gat cat ctc tca agg ata gat att agc ttt ctc ctg   2208
164 Tyr Ile Tyr Val Asp His Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu
165                 685                 690                 695
166 gat gtg agc tca ctc agc aga gcg gaa gag gac ctc agt atc aca gtg   2256
167 Asp Val Ser Ser Leu Ser Arg Ala Glu Glu Asp Leu Ser Ile Thr Val
168                 700                 705                 710
169 cat gct acc tgt gaa aat gaa gag gaa atg gac aat cta aag cac agc   2304
170 His Ala Thr Cys Glu Asn Glu Glu Glu Met Asp Asn Leu Lys His Ser
171         715                 720                 725
172 aga gtg act gta gca ata cct tta aaa tat gag gtt aag ctg act gtt   2352
173 Arg Val Thr Val Ala Ile Pro Leu Lys Tyr Glu Val Lys Leu Thr Val
174 730                 735                 740                 745
175 cat ggg ttt gta aac cca act tca ttt gtg tat gga tca aat gat gaa   2400
176 His Gly Phe Val Asn Pro Thr Ser Phe Val Tyr Gly Ser Asn Asp Glu
177                 750                 755                 760
178 aat gag cct gaa acg tgc atg gtg gag aaa atg aac tta act ttc cat   2448
179 Asn Glu Pro Glu Thr Cys Met Val Glu Lys Met Asn Leu Thr Phe His
180                 765                 770                 775
181 gtt atc aac act ggc aat agt atg gct ccc aat gtt agt gtg gaa ata   2496
182 Val Ile Asn Thr Gly Asn Ser Met Ala Pro Asn Val Ser Val Glu Ile
183                 780                 785                 790
```

E-->
```
184 atg gta cca aat tct ttt agc ccc caa act gat aag ctg ttc aac att   2588  2544
185 Met Val Pro Asn Ser Phe Ser Pro Gln Thr Asp Lys Leu Phe Asn Ile
186         795                 800                 805
187 ttg gat gtc cag act act act gga gaa tgc cac ttt gaa aat tat caa   2592
188 Leu Asp Val Gln Thr Thr Thr Gly Glu Cys His Phe Glu Asn Tyr Gln
189 810                 815                 820                 825
190 aga gtg tgt gca tta gag cag caa aag agt gca atg cag acc ttg aaa   2640
191 Arg Val Cys Ala Leu Glu Gln Gln Lys Ser Ala Met Gln Thr Leu Lys
192                 830                 835                 840
193 ggc ata gtc cgg ttc ttg tcc aag act gat aag agg cta ttg tac tgc   2688
194 Gly Ile Val Arg Phe Leu Ser Lys Thr Asp Lys Arg Leu Leu Tyr Cys
```

RAW SEQUENCE LISTING   DATE: 07/18/2000
PATENT APPLICATION: US/09/155,514A   TIME: 13:51:00

Input Set : A:\09155514.app
Output Set: N:\CRF3\07182000\I155514A.raw

```
195            845            850            855
196 ata aaa gct gat cca cat tgt tta aat ttc ttg tgt aat ttt ggg aaa   2736
197 Ile Lys Ala Asp Pro His Cys Leu Asn Phe Leu Cys Asn Phe Gly Lys
198         860            865            870
199 atg gaa agt gga aaa gaa gcc agt gtt cat atc caa ctg gaa ggc cgg   2784
200 Met Glu Ser Gly Lys Glu Ala Ser Val His Ile Gln Leu Glu Gly Arg
201     875            880            885
202 cca tcc att tta gaa atg gat gag act tca gca ctc aag ttt gaa ata   2832
203 Pro Ser Ile Leu Glu Met Asp Glu Thr Ser Ala Leu Lys Phe Glu Ile
204 890            895            900            905
205 aga gca aca ggt ttt cca gag cca aat cca gta att gaa cta aac       2880
206 Arg Ala Thr Gly Phe Pro Glu Pro Asn Pro Arg Val Ile Glu Leu Asn
207            910            915            920
208 aag gat gag aat gtt gcg cat gtt cta ctg gaa gga cta cat cat caa   2928
209 Lys Asp Glu Asn Val Ala His Val Leu Leu Glu Gly Leu His His Gln
210            925            930            935
211 aga ccc aaa cgt tat ttc acg gat ccc gag ctgctggaag caggctcagc    2978
212 Arg Pro Lys Arg Tyr Phe Thr Asp Pro Glu
213            940            945
214 gctcctgcct ggacgcatcc cggctatgca gccccagtcc agggcagcaa ggcaggcccc 3038
215 gtctgcctct tcacccggag cctctgcccg ccccactcat gctcagggag agggtcttct 3098
216 ggcttttttcc caggctctgg gcaggcacag gctaggtgcc cctaacccag gccctgcaca 3158
217 caaaggggca ggtgctgggc tcagacctgc caagagccat atccgggagg accctgcccc 3218
218 tgacctaagc ccaccccaaa ggccaaactc tccactccct cagctcggac accttctctc 3278
219 ctcccagatt ccagtaactc ccaatcttct ctctgca gag ccc aaa tct tgt gac  3333
220                                         Glu Pro Lys Ser Cys Asp
221                                                     950
222 aaa act cac aca tgc cca ccg tgc cca ggtaagccag cccaggcctc        3380
223 Lys Thr His Thr Cys Pro Pro Cys Pro
224     955            960
225 gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcatccagg gacaggcccc 3440
226 agccgggtgc tgacacgtcc acctccatct cttcctca gca cct gaa ctc ctg     3493
227                                         Ala Pro Glu Leu Leu
228                                                     965
229 ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc   3541
230 Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
231         970            975            980
232 atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc   3589
233 Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
234     985            990            995
235 cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag   3637
236 His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
237 1000            1005            1010            1015
238 gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg   3685
239 Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
240            1020            1025            1030
241 tac cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat   3733
242 Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
243            1035            1040            1045
```

```
244 ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc   3781
245 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
246       1050          1055              1060
247 atc gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtggggtgcg        3828
248 Ile Glu Lys Thr Ile Ser Lys Ala Lys
249     1065           1070
250 agggccacat ggacagaggc cggctcggcc caccctctgc cctgagagtg accgctgtac 3888
252 caacctctgt cctaca ggg cag ccc cga gaa cca cag gtg tac acc ctg     3937
253                Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
254                   1075              1080
255 ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc   3985
256 Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
257   1085              1090              1095
258 ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc   4033
259 Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
260 1100          1105              1110              1115
261 aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gat   4081
262 Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
263           1120              1125              1130
264 tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc   4129
265 Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
266           1135              1140              1145
267 agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct   4177
268 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
269   1150              1155              1160
270 ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa   4225
271 Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
272   1165              1170              1175
273 tga                                                             4228
```

VERIFICATION SUMMARY   DATE: 07/18/2000
PATENT APPLICATION: US/09/155,514A   TIME: 13:51:02

Input Set : A:\09155514.app
Output Set: N:\CRF3\07182000\I155514A.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier
L:7 M:283 W: Missing Blank Line separator, <130> field identifier
L:8 M:282 W: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.
L:8 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:283 W: Missing Blank Line separator, <160> field identifier
L:184 M:254 E: No. of Bases conflict, LENGTH:Input:2588 Counted:2544 SEQ:1
L:505 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:507 M:283 W: Missing Blank Line separator, <400> field identifier
L:516 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:528 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:541 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:554 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:566 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:578 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:590 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:602 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:612 M:283 W: Missing Blank Line separator, <220> field identifier
L:613 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:615 M:283 W: Missing Blank Line separator, <400> field identifier
L:625 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:637 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:651 M:283 W: Missing Blank Line separator, <400> field identifier
L:660 M:283 W: Missing Blank Line separator, <220> field identifier
L:660 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:663 M:283 W: Missing Blank Line separator, <400> field identifier
L:672 M:283 W: Missing Blank Line separator, <220> field identifier
L:672 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:968 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:980 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:992 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:1004 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:1041 M:256 W: Invalid Numeric Header Field, <220> has non-blank data